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L10: Entry 13 of 13

File: USPT

Mar 29, 1994

DOCUMENT-IDENTIFIER: US 5298422 A
TITLE: Myogenic vector systems

DATE FILED (1):
19911106

Brief Summary Text (25):
For specific embodiments the cassette contains the nucleic acid sequence for the insulin like growth factor I, insulin like growth factor II, insulin growth factor binding protein, growth hormone releasing factor, apolipoprotein A-1 or a protein capable of inducing an antibody response.

Detailed Description Text (10):
The 3' untranslated region of the chicken skeletal alpha actin gene which starts at nucleotide 2060 and extends to 2331. The complete 3' untranslated region and contiguous noncoding DNA extends an additional 2.0 Kb. This 2.3 Kb fragment can be linked immediately following the natural translation termination codon to a copy DNA sequence coding for a polypeptide desired to be expressed.

CLAIMS:

17. The MVS of claim 1, 3 or 8, wherein the expressed nucleic acid sequence codes for insulin like growth factor I, insulin like growth factor II or insulin growth factor binding protein.

20. The MVS of claim 11, wherein the expressed nucleic acid sequence codes for insulin like growth factor I, insulin like growth factor II or insulin growth factor binding protein.

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L10: Entry 12 of 13

File: USPT

May 26, 1998

DOCUMENT-IDENTIFIER: US 5756264 A
TITLE: Expression vector systems and method of use

DATE FILED (1):
19940309

Brief Summary Text (40):
Specific examples of these compounds include proinsulin, insulin, growth hormone, growth hormone release factor, androgen receptors, insulin-like growth factor I, insulin-like growth factor II, insulin-like growth factor binding protein, erythropoietin, clotting factors (VII, VIII, IX, others), chorionic gonadotropin, prolactin, endorphin, enkephalins, epidermal growth factor, TGF-.alpha., TGF-.beta., nerve growth factors, dermal growth factor (PDGF), angiogenesis factors (e.g., acidic fibroblast growth factor, basic fibroblast growth factor and angiogenin), antiangiogenesis factors (interferon-.alpha., interferon-.beta., interferon-.gamma., thrombospondin), brain growth factors, ciliary growth factors, matrix proteins (e.g., type IV collagen, type VII collagen, laminin), oncogenes (e.g., ras, fos, myc, erb, src, sis, jun), E6 or E7 transforming sequence, p53 protein, dystrophin, cytokinereceptors, interleukins (IL-1, IL-2, IL-4, IL-6, IL-8, IL-10, IL-12), interleukin inhibitors, viral capsid protein, viral reverse transcriptase, HIV-encoded protein, and antigens from eukaryotic, viral, bacterial, fungal, yeast, and parasitic organisms which can be used to induce an immunologic response.

Brief Summary Text (47):
In a preferred embodiment, the vector described above may have its 5' flanking region and/or its 3' flanking region from myogenic genes, in particular the skeletal .alpha.-actin gene. The 3'UTR of the chicken skeletal .alpha.-actin gene starts at nucleotide 2060 and extends to 2331 (Sequence I.D. No. 1), approximately 0.3 Kb. The complete 3' flanking region with a 3'UTR and contiguous 3' NCR of the gene extends an additional 2.0 Kb. This 2.3 Kb fragment can be linked immediately following the natural translation termination codon to a cDNA sequence coding for the protein or RNA to be expressed. As discussed above, these regions can be further and more precisely defined by routine methodology, e.g. deletion or mutation analysis or their equivalents. Preferably, the vector contains such a 3' region or 5' region comprising, consisting, or consisting essentially of the regions disclosed above. The terms "comprising," "consisting," or "consisting essentially of" as used herein (with respect to a vector with the 3' or 5' regions of the present invention) includes those regions as well as those regions above in which the sequence is changed but the desired vector activity remains equivalent. Such a change, for example, could be a change of ten nucleotides in any of the above regions. This is only an example and is non-limiting.

Brief Summary Text (58):
A fifth related aspect of the present invention features a method for treating disease by transfecting cells with the above-referenced vectors. Disease can include but is not limited to muscle atrophy, atherogenesis, atherosclerotic cardiovascular, cerebrovascular, or peripheral vascular disease, diabetes, neuropathy, growth disorders and hemophilia. These vectors contain nucleic acid sequences coding for proteins or RNA. The sequences can encode for insulinlike growth factor I, insulin-like growth factor II, insulin growth factor binding protein, growth hormone, growth hormone release hormone, androgen receptors, mutant androgen receptors or derivatives thereof, apolipoprotein A-I, lipoprotein lipase, or the VLDL-receptor, nerve growth factor, or brain derived neurotropic factors. These are only examples and are not meant to be limiting. "Receptor" as used herein includes natural receptors (i.e., as found in a cell *in vivo*) as well as anything that binds alike and causes compartmentalization changes in a cell.

1 agggacgctg ccgcaccgcc ccagtttacc ccggggagcc atcatgaagc
51 tgaatggcca ccagttggag aaccatgccc tgaaggcttc ctacatcccc
101 gatgagcaga tagcacaggg acctgagaat gggcgccgag ggggcttgg
151 ctctcggggt cagccccccc agggctcacc tggcgcagcg gggggcccccag
201 ccaagcagca gcaagtggac atcccccttc ggctcctggt gcccacccag
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301 aaaacagacc cagtccaaga tagacgtca taggaaggag aacgcaggtg
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1701 ttttaaaa

SEQ ID NO; 5



formatting BLAST

Translations Retrieve results for an RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (1708 letters)

The request ID is **1037229979-01300-25298**

Format! or **Reset all**

The results are estimated to be ready in 38 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show Graphical Overview Linkout Sequence Retrieval NCBI-g Alignment in **HTML**

Number of: **Descriptions** **100** **Alignments** **50**

Alignment view **Pairwise**

Limit results by **entrez query** **(none)** or select from: **(none)**

Expect value **range:**

4191608|gb|AAD09826.1| IGF-II mRNA-binding protein 1 [Homo sapiens]
Length = 577

Score = 829 bits (2141), Expect = 0.0
Identities = 428/445 (96%), Positives = 428/445 (96%), Gaps = 2/445 (0%)
Frame = +2

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R AIMKLNHGQLENHALKVSYIPDEQIAQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ
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Query: 572 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAA 745
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Query: 746 VGLFXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKQHICKQLS 925
VGLF TGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKQHICKQLS
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Query: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105
RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI
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Query: 1106 RVPASAAGRIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 1285
RVPASAAGRIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK
Sbjct: 493 RVPASAAGRIGKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRK 552

Query: 1286 IRDILAQVKQQHQKGQSNSQAQARRK 1360
IRDILAQVKQQHQKGQSNSQAQARRK
Sbjct: 553 IRDILAQVKQQHQKGQSNSQAQARRK 577

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725 391 187
22-mr 187
>gi|21361352|ref|NP_006537.2| IGF-II mRNA-binding protein 1 [Homo sapiens]
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Length = 577

Score = 825 bits (2131), Expect = 0.0
Identities = 426/445 (95%), Positives = 426/445 (95%), Gaps = 2/445 (0%)
Frame = +2

Query: 32 RGAIMKLNHGQLENHALKVSYIPDEQIAQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ 211
R AIMKLNHGQLENHALKVSYIPDEQIAQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ
Sbjct: 133 RQAIMKLNHGQLENHALKVSYIPDEQIAQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ 192

Query: 212 QVDIPLRLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391
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Query: 572 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAA 745
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 Sbjct: 313 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMSLQSHLTPGLNLAA 372

Query: 746 VGLFXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS 925
 VGLF TGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS
 Sbjct: 373 VGLFPASSSAVPPPPSSVTGAAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKQHIKQLS 432

Query: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105
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Query: 1106 RVPASAAGRVIDKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 1285
 RVPASAAGRVIDKGGKTVNELQNLTAEEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK
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Query: 1286 IRDILAQVKQQHQKGQSNQAOARRK 1360
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 Sbjct: 553 IRDILAQVKQQHQKGQSNQAOARRK 577

>gi|6753518|ref|NP_034081.1| insulin-like growth factor 2, binding protein 1; coding region
 determinant binding protein; zipcode-binding protein 1;
 zipcode binding protein 1 [Mus musculus]
 gi|3273749|gb|AAC72743.1| coding region determinant binding protein [Mus musculus]
 gi|12851514|dbj|BAB29071.1| coding region determinant binding protein~data source:MGD, source
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 Length = 577

Score = 822 bits (2123), Expect = 0.0
 Identities = 424/445 (95%), Positives = 425/445 (95%), Gaps = 2/445 (0%)
 Frame = +2

Query: 32 RGAIMKLNHGQLENHALKVSYIPDEQIAQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ 211
 R AIMKLNHGQLENHALKVSYIPDEQI QGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ
 Sbjct: 133 RQAIMKLNHGQLENHALKVSYIPDEQITQGPENGRRGGFGSRGQPRQGS PVAAGAPAKQQ 192

Query: 212 QVDIPLRLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 391
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Sbjct: 193 PVDIPLRLVPTQYVGAIIGKEGATIRNITKQTQSKIDVHRKENAGAAEKAISVHSTPEG 252

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Query: 572 SSLQDLTLYNPERTITVKGAIENCCRAEQEIMKKVREAYENDVAAMS--SHLIPGLNLAA 745
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Query: 746 VGLFXXXXXXXXXXXXXTGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKGQHIKQLS 925
VGLF TGAAPYSSFMQAPEQEMVQVFIPAPAQAVGAIIGKKGQHIKQLS

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Query: 926 RFASASIKIAPPETPDSKVRMVIITGPPEAQFKAQGRIYGKLKEENFFGPKEEVKLETHI 1105
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Query: 1106 RVPASAAGRVIDGGKTVNELQNLAAEVVVPRDQTPDENDQVIVKIIIGHFYASQMAQRK 1285
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[Mus musculus]

Length = 441